```
!!NA_SEQUENCE 1.0
ID   AI113131    standard; RNA; EST; 315 BP.
XX
AC   AI113131;
XX
SV   AI113131.1
XX
DT   04-SEP-1998 (Rel. 56, Created)
DT   15-MAR-1999 (Rel. 59, Last updated, Version 2)
XX
DE   UI-R-C2p-nr-f-06-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone
DE   UI-R-C2p-nr-f-06-0-UI 3', mRNA sequence.
XX
KW   EST.
XX
OS   Rattus norvegicus (Norway rat)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
OC   Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

XX
RN   [1]
RP   1-315
RX   MEDLINE; 97044477.
RA   Bonaldo M.F., Lennon G., Soares M.B.;
RT   "Normalization and subtraction: two approaches to facilitate gene
RT   discovery";
RL   Genome Res. 6(9):791-806(1996).
XX
CC   Contact: Soares, MB
CC   Program for Rat Gene Discovery and Mapping
CC   University of Iowa
CC   451 Eckstein Medical Research Building Iowa City, IA 52242, USA
CC   Tel: 319 335 8250
CC   Fax: 319 335 9565
CC   Email: msoares@blue.weeg.uiowa.edu
CC   Oligo-dT track not found, Not I site shown in beginning of sequence
CC   is likely internal to the message. cDNA Library Preparation: M.
CC   Fatima Bonaldo, Ph.D. Clone distribution: clones will be available

CC   through Research Genetics The following repetitive elements were
CC   found in this cDNA sequence: 97-125, >GC_rich#Low_complexity
CC   Seq primer: M13 Forward.
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .315
FT                   /db_xref="taxon:10116"
FT                   /db_xref="ESTLIB:1413"
FT                   /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT                   polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
FT                   library is a subtracted library derived from the UI-R-C1
FT                   library, which is a subtracted library derived from the

FT                   UI-R-C0 library.  The UI-R-C0 library consisted of a
FT                   mixture of individually tagged normalized  libraries
FT                   constructed from rat placenta, adult lung, brain, liver,
FT                   kidney,  heart, spleen, ovary, muscle, 8, 12 and 18-day
```

FT   idecification of the library of origin of a clone within
FT   the mixture. The subtracted library (UI-R-C2p) was
FT   constructed as follows: PCR amplified cDNA inserts from

FT   UI-R-C1 clones from which 3' ESTs had been derived was us

FT   as a driver in a hybridization with the UI-R-C1 library i
FT   the form of single-stranded circles. The remaining
FT   single-stranded circles (subtracted library) was purified
FT   by hydroxyapatite column chromatography, converted to
FT   double-stranded circles and electroporated into DH10B
FT   bacteria (Life Technologies) to generate the UI-R-C2p
FT   library. This procedure has been previously described
FT   (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,

FT   1996)"
FT   /organism="Rattus norvegicus"
FT   /strain="Sprague-Dawley"
FT   /clone="UI-R-C2p-nr-f-06-0-UI"
FT   /clone_lib="UI-R-C2p"
FT   /dev_stage="adult"
FT   /lab_host="DH10B (Life Technologies)"
XX
SQ   Sequence 315 BP; 46 A; 110 C; 116 G; 43 T; 0 other;

Ai113131 Length: 315 March 20, 19100 09:52 Type: N Check: 7433 ..

      1 CGGGCGCACG GTCTCAGGTC CGAAGTCCCT GAGCTCCGAC TGGTTGTTGA

     51 AGCGGGTGAG GCGCTTGCAC TTGCACGAGG CCACCATACG CACCTTGCGC

    101 GAGCGCCGCG CCGCGCCGCC GGGGCACAGC AGCTGCACCC GCTGCGCGCG

    151 GTAGCGATCC GGGATGCAGC GGAAGTCGGG TCCGTTCGGG CGCCACCACT

    201 TCACGCGCCC GATGGCGTTG GGCAGCAGCC GCGCGGGGCC GCACTGGCCC

    251 GAGCACACCA ACTCGGTGAC CGGCTTGGCA CTGCGGCACG GGCCGTCGGT

    301 CACGAAGCGG GTGTA

```
!!NA_SEQUENCE 1.0
ID    HS1222641   standard; RNA; EST; 180 BP.
XX
AC    AA393939;
XX
SV    AA393939.1
XX
DT    19-MAY-1997 (Rel. 51, Created)
DT    19-MAY-1997 (Rel. 51, Last updated, Version 1)
XX
DE    zv64f09.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
DE    758441 5'.
XX
KW    EST.
XX
OS    Homo sapiens (human)
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
OC    Primates; Catarrhini; Hominidae; Homo.
XX
RN    [1]
RP    1-180

RA    Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S., Kucaba T

RA    Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K.
RA    Steptoe M., Tan F., Theising B., White Y., Wylie T., Waterston R.,
RA    Wilson R.;
RT    "WashU-Merck EST Project 1997";
RL    Unpublished.
XX
DR    RZPD; IMAGp998G181865Q6; 16-Jul-1999.
XX
CC    Contact: Wilson RK WashU-Merck EST Project Washington University
CC    School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC    MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC    est@watson.wustl.edu This clone is available royalty-free through
CC    LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for

CC    further information. Putative full length read The vector to vector
CC    length is Seq primer: -28m13 rev2 ET from Amersham.
XX
FH    Key             Location/Qualifiers
FH
FT    source          1. .180
FT                    /db_xref="taxon:9606"
FT                    /db_xref="ESTLIB:843"
FT                    /db_xref="RZPD:IMAGp998G181865Q6"
FT                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT                    polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT                    was prepared from mRNA obtained from pooled 8-9 week
FT                    (total) fetus material with a Not I - oligo(dT) primer [5'

FT                    TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAATTTTTTTTTTTTTTTTT 3'].
FT                    Double-stranded cDNA was ligated to Eco RI adaptors
FT                    (Pharmacia), digested with Not I and cloned into the Not I
FT                    and Eco RI sites of the modified pT7T3 vector. Library wer
```

```
. FT                        through one round of normalization, and was constructed
FT                          Bento Soares and M. Fatima Bonaldo."
FT                          /organism="Homo sapiens"
FT                          /clone="758441"
FT                          /clone_lib="Soares total fetus Nb2HF8 9w"
FT                          /dev_stage="8-9 weeks"

FT                          /lab_host="DH10B"
FT      mRNA                <1. .>180
XX
SQ      Sequence 180 BP; 61 A; 27 C; 55 G; 37 T; 0 other;

Hs1222641  Length: 180  March 17, 19100 09:46  Type: N  Check: 9094  ..

        1  GAGAGAGAGA GAGAAAGAGA CTATTGGCAT ATGATTCCAA GGACTCCAGT

       51  GCCAGTTGAA TGGGCAGAGG TGAGAGAGAG AGAGAGAAAG AGAGAGAATG

      101  AATGCAGTTG CATTGATTCA GTGCCAAGGT CACTTCCAGA ATTCAGAGTT

      151  GTGATGCTCT CTTCTGACAG CCAAAGATGA
```

```
ID      AC003098     standard; DNA; HUM; 94752 BP.
AC      AC003098;
SV      AC003098.1
DT      14-NOV-1997 (Rel. 53, Created)
DT      05-JUL-1999 (Rel. 60, Last updated, Version 11)
DE      Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.
KW      HTG.
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
OC      Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      1-94752
RA      Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P., Lander E.;
RT      "Homo sapiens chromosome 17, clone HRPC905N1";
RL      Unpublished.
RN      [2]
RP      1-94752
RA      Birren B., Fasman K., McKernan K., Munro C., Nusbaum C., Richardson P.,
RA      Lander E., Baldwin J., Barna N., Cantu C., Chang A., Cooke P., Daly M.J.
RA      Devon K., Dewar K., DuRette B., Forrest C., Gage D., Gensheimer S.,
RA      Geraigery K., Gilmartin T., Hagos B., Halphen I., Harris K., Howland J.C
RA      Huang J., Hui L., Jacotot L., Kirby A., Lane M., MacKenzie J., Marquis N
RA      McDermott J., Molla M., Morrow J., Nachman A., Naylor J., O'Connor T.,
RA      Olotu A., Peterson K., Roberts D., Rollins G., Sarnaik A., Shiu P.,
RA      Shyam R., Stilwell J., Stone C., Strickland C., Sydney K., Tang L.,
RA      Zemtseva I., Zody M.;
RT      ;
RL      Submitted (10-NOV-1997) to the EMBL/GenBank/DDBJ databases.

RL      Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
RL      Cambridge, MA 02141, USA
RN      [3]
RP      1-94752
RA      Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P., Lander E.,
RA      Allen N., Baker J., Baldwin J., Barna N., Beckerly R., Boutwell C.,
RA      Byrne S., Cantu C., Castle A., Cooke P., Daly M.J., Depayre E., Devon K.,
RA      Dewar K., DuRette B., Etemadi S., Ferreira P., Forrest C., Gage D.,
RA      Gardyna S., Gensheimer S., Geraigery K., Gilmartin T., Gray D., Hagos B.
RA      Harris K., Horton L., Howland J.C., Hui L., Jacotot L., Linton L.,
RA      MacKenzie J., Marquis N., McEwan P., McGurk A., Meldrim J., Molla M.,

RA      Morris W., Morrow J., Nachman A., Naylor J., O'Connor T., Pavlin B.,
RA      Peterson K., Ranganath S., Riley R., Roberts D., Rollins G., Rossello R.,
RA      Roy A., Shyam R., Soohoo S., Stilwell J., Stone C., Strickland C.,
RA      Sydney K., Tang L., Vassiliev H., Vo A., Wagner A., Wheeler J., Wu Y.,
RA      Ye W.J., Zemtseva I., Zhao J., Zody M.;
RT      ;
RL      Submitted (29-JAN-1998) to the EMBL/GenBank/DDBJ databases.
RL      Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
RL      Cambridge, MA 02141, USA
CC      All repeats were identified using RepeatMasker: Smit, A.F.A. &
CC      Green, P. (1996-1997) . . .
```

SCORES   Init1: 10214 Initn: 10214 Opt: 10221 z-score: 3674.2 E():
99.4% identity in 2073 bp overlap


```
                                 2299        2289        2279
Sa263085_000                     CTTTCGGTCATGATTCATTGTCTTTATTAA
                                 ||||||||||||||||||||||||||||||
Ac003098       CATGTGTGGTTGACAAAATGAGACCACATCCTTTCGGTCATGATTCATTGTCTTTATTAA
                 4230        4240        4250        4260        4270        4280


               2269        2259        2249        2239        2229        2219
Sa263085_000   CAATGTCTCTGGACTCTGGAAGAACAGACTGTTAATTCATAAAGCAATATTAACATTGTC

               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       CAATGTCTCTGGACTCTGGAAGAACAGACTGTTAATTCATAAAGCAATATTAACATTGTC
                 4290        4300        4310        4320        4330        4340


               2209        2199        2189        2179        2169        2159
Sa263085_000   ATTCTCTACAAGAAAAACTTTTGCATAAATAACTTAAGTGAGAAAATAAATATGTAACTT
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       ATTCTCTACAAGAAAAACTTTTGCATAAATAACTTAAGTGAGAAAATAAATATGTAACTT
                 4350        4360        4370        4380        4390        4400


               2149        2139        2129        2119        2109        2099
Sa263085_000   AACTCTTTAAAAACCACTACTTTCATTCTTGTGGACAAGTCCCACGTGGAAGAATTGCCA
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       AACTCTTTAAAAACCACTACTTTCATTCTTGTGGACAAGTCCCACGTGGAAGAATTGCCA
                 4410        4420        4430        4440        4450        4460


               2089        2079        2069        2059        2049        2039
Sa263085_000   AAAAAACGACCAGTCCTGCAGGCTTTCATATGTCATGTGCTTCTGTTTAAAACTTTTTTT
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       AAAAAACGACCAGTCCTGCAGGCTTTCATATGTCATGTGCTTCTGTTTAAAACTTTTTTT
                 4470        4480        4490        4500        4510        4520


               2029        2019        2009        1999        1989        1979
Sa263085_000   TTTTAACAATTAAAAACTACACAGAAAGTAAGAGGTTGTCTGGAAATGATTTTCAAAAAG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       TTTTAACAATTAAAAACTACACAGAAAGTAAGAGGTTGTCTGGAAATGATTTTCAAAAAG
                 4530        4540        4550        4560        4570        4580


               1969        1959        1949        1939        1929        1919
Sa263085_000   ATTTTTGGGTGGCAGCTATTATGCTCTGCAGTTTCTCAGCATATGTACAGCACTTGTAGT
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       ATTTTTGGGTGGCAGCTATTATGCTCTGCAGTTTCTCAGCATATGTACAGCACTTGTAGT
                 4590        4600        4610        4620        4630        4640


               1909        1899        1889        1879        1869        1859
Sa263085_000   TTTTCCCCCAATAATATTCTTTTAGTGTAAGATATGCCATCACATGTAAGAGCAGTAAGA
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       TTTTCCCCCAATAATATTCTTTTAGTGTAAGATATGCCATCACATGTAAGAGCAGTAAGA
                 4650        4660        4670        4680        4690        4700


               1849        1839        1829        1819        1809        1799
Sa263085_000   AGCTGTTTTCTAGGCAGAAATGTGTCCGTGAGTGGTGGGCAGAAGGCGGTGTCTCAAAAG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098       AGCTGTTTTCTAGGCAGAAATGTGTCCGTGAGTGGTGGGCAGAAGGCGGTGTCTCAAAAG
```

```
                1789          779         1769          1759          1749          1739
Sa263085_000  GGATGTGCTGGTCTGTGAGTTTGTGATGGCTGCTCCCTCGGGCCTGCAAGGCCAGTGTCC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GGATGTGCTGGTCTGTGAGTTTGTGATGGCTGCTCCCTCGGGCCTGCAAGGCCAGTGTCC
                4770          4780          4790          4800          4810          4820


                1729          1719          1709          1699          1689          1679
Sa263085_000  TTGAACCTTTCACTTCTCTTCGGAAGGTGACTTTAAAACATGGCTATGGGTCGGGGGAGG

              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      TTGAACCTTTCACTTCTCTTCGGAAGGTGACTTTAAAACATGGCTATGGGTCGGGGGAGG
                4830          4840          4850          4860          4870          4880


                1669          1659          1649          1639          1629          1619
Sa263085_000  GATGCTGCTCTTTGGGAAGTTGGGGCGGATGTGATTTCTATCCCTCCCACCACCCTCGGA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GATGCTGCTCTTTGGGAAGTTGGGGCGGATGTGATTTCTATCCCTCCCACCACCCTCGGA
                4890          4900          4910          4920          4930          4940


                1609          1599          1589          1579          1569          1559
Sa263085_000  CCCTCTCCTTTTCTACCCCAATGGATGATGTTATTTCTTTGAGATGGAGGGGTGGAGGTA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CCCTCTCCTTTTCTACCCCAATGGATGATGTTATTTCTTTGAGATGGAGGGGTGGAGGTA
                4950          4960          4970          4980          4990          5000


                1549          1539          1529          1519          1509          1499
Sa263085_000  GCCAAACATCCGGGGAAGCCAGGCTGGGAAGCAGCATAGCTTCTTCCAGGAGTTTGTCAG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GCCAAACATCCGGGGAAGCCAGGCTGGGAAGCAGCATAGCTTCTTCCAGGAGTTTGTCAG
                5010          5020          5030          5040          5050          5060


                1489          1479          1469          1459          1449          1439
Sa263085_000  CCGTAAATATGTCAGCCATAAATAGACTCTTTACTTTTTTTTTTCTGTTTGTTTTTCATC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CCGTAAATATGTCAGCCATAAATAGACTCTTTACTTTTTTTTTTCTGTTTGTTTTTCATC
                5070          5080          5090          5100          5110          5120


                1429          1419          1409          1399          1389          1379
Sa263085_000  TTTGGCTGTCAGAAGAGAGCATCACAACTCTGAATTCTGGAAGTGACCTTGGCACTGAAT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      TTTGGCTGTCAGAAGAGAGCATCACAACTCTGAATTCTGGAAGTGACCTTGGCACTGAAT

                5130          5140          5150          5160          5170          5180


                1369          1359          1349          1339          1329          1319
Sa263085_000  CAATGCAACTGCATTCATTCTCTCTCTTTCTCTCTCTCTCTCACCTCTGCCCATTCAA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CAATGCAACTGCATTCATTCTCTCTCTTTCTCTCTCTCTCTCACCTCTGCCCATTCAA
                5190          5200          5210          5220          5230          5240


                1309          1299          1289          1279          1269          1259
Sa263085_000  AAGGCACTGGAGTCCTTGGAATCATATGCCAATAGTCTCCTCGAGATCCTATTCCCACCT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Ac003098      AAGGCACTGGAGTCCTTGGAATCATATGCCAATAGTCTCCTCGAGATCCTATTCCCACCT
                5250          5260          5270          5280          5290          5300
```

```
                    1249      1239      1229      1219      1209      1199
Sa263085_000  CCACCCTCATTTTACAAAGTGGAAATTGAGGTCCCGAAGGAGAATTGTGTAGTTCAAGGT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CCACCCTCATTTTACAAAGTGGAAATTGAGGTCCCGAAGGAGAATTGTGTAGTTCAAGGT
                    5310      5320      5330      5340      5350      5360

                    1189      1179      1169      1159      1149      1139
Sa263085_000  TACACAGCAAGTTAGTGGCAGAGCCAGGACTAGAAACCACATCTACAGTTGCCCCCAGTC

              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      TACACAGCAAGTTAGTGGCAGAGCCAGGACTAGAAACCACATCTACAGTTGCCCCCAGTC
                    5370      5380      5390      5400      5410      5420

                    1129      1119      1109      1099      1089      1079
Sa263085_000  TTGTGCTCTGGGCACGCCTCAGGCTTTCTGATGGGCAGCGAGGTGCAAGGGGGAATCTTA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      TTGTGCTCTGGGCACGCCTCAGGCTTTCTGATGGGCAGCGAGGTGCAAGGGGGAATCTTA
                    5430      5440      5450      5460      5470      5480

                    1069      1059      1049      1039      1029      1019
Sa263085_000  TCCAACTTTCTTAACCAGTCCCTGGACTTTCCCACTCCCACACCGCTCCCTTAAAACCCC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      TCCAACTTTCTTAACCAGTCCCTGGACTTTCCCACTCCCACACCGCTCCCTTAAAACCCC
                    5490      5500      5510      5520      5530      5540

                    1009       999       989       979       969       959
Sa263085_000  AGGGCGGTGAAAATGCTTCCATTTCTGCCTCCTCTGAAGTGGGACCAGCAAAGGTAGGCG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      AGGGCGGTGAAAATGCTTCCATTTCTGCCTCCTCTGAAGTGGGACCAGCAAAGGTAGGCG
                    5550      5560      5570      5580      5590      5600

                     949       939       929       919       909       899
Sa263085_000  GCCCCAGAGGCGGGGCTGCGTGGCTCAGTGTCTGTGACTCTCAATTCCCTCCCCTGCCCC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GCCCCAGAGGCGGGGCTGCGTGGCTCAGTGTCTGTGACTCTCAATTCCCTCCCCTGCCCC
                    5610      5620      5630      5640      5650      5660

                     889       879       869       859       849       839
Sa263085_000  GTGGGACCCCTCAGCTGGCGGGCTGAGGGGGGCCTTGCCGGCGCCCGGGATTCCTCAGGG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      GTGGGACCCCTCAGCTGGCGGGCTGAGGGGGGCCTTGCCGGCGCCCGGGATTCCTCAGGG
                    5670      5680      5690      5700      5710      5720

                     829       819       809       799       789       779
Sa263085_000  CCTGGAAGGTCTCAGCCCCCTGCCCTGGGTTGCAGGCATTTACAATGAAATATAAACAAT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CCTGGAAGGTCTCAGCCCCCTGCCCTGGGTTGCAGGCATTTACAATGAAATATAAACAAT
                    5730      5740      5750      5760      5770      5780

                     769       759       749       739       729       719
Sa263085_000  CAAACCACGCGCAGAGGACAGAAATGTGGGGCGCGGGTTCAGGGCCGGGGCGCCCGCCGG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ac003098      CAAACCACGCGCAGAGGACAGAAATGTGGGGCGCGGGTTCAGGGCCGGGGCGCCCGCCGG
                    5790      5800      5810      5820      5830      5840
```

```
                709        699        689        679        669        659
  Sa263085_000 TGGGGAGGGGCGCGGGCGGGCTCTAGTAGGCGTTCTCCAGCTCGGCCTGGTTGGCTTTGG
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      Ac003098 TGGGGAGGGGCGCGGGCGGGCTCTAGTAGGCGTTCTCCAGCTCGGCCTGGTTGGCTTTGG
                5850       5860       5870       5880       5890       5900

                649        639        629        619        609        599
  Sa263085_000 CGCTCCGGGCGCGGGGCCGCGGCTTCCGGCCCTTCTGCGGCCGAGCGGCCTCGGTCCCGA

                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      Ac003098 CGCTCCGGGCGCGGGGCCGCGGCTTCCGGCCCTTCTGCGGCCGAGCGGCCTCGGTCCCGA
                5910       5920       5930       5940       5950       5960

                589        579        569        559        549        539
  Sa263085_000 AGTCCTTGAGCTCCGACTGGTTGTGGAAGCGGGTGAGGCGCTTGCACTTGCACGAGGCCA
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      Ac003098 AGTCCTTGAGCTCCGACTGGTTGTGGAAGCGGGTGAGGCGCTTGCACTTGCACGAGGCCA
                5970       5980       5990       6000       6010       6020

                529        519        509        499        489        479
  Sa263085_000 CCAGGCGCACCTTGCGCGCGCGCGGCGCCTCACCACCGGGACACAGCAGCTGCACGCGCT
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      Ac003098 CCAGGCGCACCTTGCGCGCGCGCGGCGCCTCACCACCGGGACACAGCAGCTGCACGCGCT
                6030       6040       6050       6060       6070       6080

                469        459        449        439        429        419
  Sa263085_000 GCGCGCGGTAGCGGTCGGGGATGCAGCGGAAGTCGGGCCCACTAGGTCGCCACCACTTGC
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      Ac003098 GCGCGCGGTAGCGGTCGGGGATGCAGCGGAAGTCGGGCCCACTAGGTCGCCACCACTTGC
                6090       6100       6110       6120       6130       6140

                409        399        389        379        369        359
  Sa263085_000 CGCGGCCGATGGCGTTGGGCAGCAGGCGCGCCGGGCCGCACTGGCCGGAGCACACCAGCT
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      Ac003098 CGCGGCCGATGGCGTTGGGCAGCAGGCGCGCCGGGCCGCACTGGCCGGAGCACACCAGCT
                6150       6160       6170       6180       6190       6200

                349        339        329        319        309        299
  Sa263085_000 CGGTGACCGGCTTGGCGCTGCGGCACGGCCCATCGGTCACGTAGCGGGTGAAGTGCAGCT
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      Ac003098 CGGTGACCGGCTTGGCGCTGCGGCACGGCCCATCGGTCACGTAGCGGGTGAAGTGCAGCT
                6210       6220       6230       6240       6250       6260

                289        279        269        259        249        239
  a263085_000 CGCGGCAGCTGTACTCGGACACGTCTTTGGTCTCAAAGGGGTG-GTG-GGGAGGCCGCCC
               |||||||||||||||||||||||||||| |||   |  ||| |  ||| ||| ||||||||
    c003098 CGCGGCAGCTGTACTCGGACACGTCTGTGG--AGAGAGGCGCGCGTGAGGGTGGCCGCCC
                6270       6280       6290       6300       6310       6320

                229        219        209        199        189        179
  a263085_000 TCCGTTCTCCGCCCGGTTCATGGTCTTGTTGTTCTCCAGCTCCGGTGGAGGCTCGGGGTA
               ||

    c003098 GCCTGGCCACCCCTGCCCTGGACCGGCCCGTCTCTCTCCACCCCAGCCCTGCTTTTGCCA
                6330       6340       6350       6360       6370       6380
```